

SEQUENCE LISTING

<110> NI ET AL.

<120> HUMAN ENDOMETRIAL SPECIFIC STEROID-BINDING FACTOR I, II AND III

<130> PF257D3

<140> Unassignend

<141> 2001-11-06

<150> 09/583,169

<151> 2000-05-30

<150> 09/263,810

<151> 1999-03-08

<150> 08/821,451

<151> 1997-03-21

<150> 60/014,724

<151> 1996-03-21

<160> 27

<170> PatentIn version 3.1

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Met Arg Leu Ser

-20

gtg tgt ctc ctg atg gtc tcg ctg gcc ctt tgc tgc tac cag gcc cat 102

Val Cys Leu Leu Met Val Ser Leu Ala Leu Cys Cys Tyr Gln Ala His

-15 -10 -5

gct ctt gtc tgc cca gct gtt gct tct gag atc aca gtc ttc tta ttc 150
Ala Leu Val Cys Pro Ala Val Ala Ser Glu Ile Thr Val Phe Leu Phe
-1 1 5 10 15

tta agt gac gct gcg gta aac ctc caa gtt gcc aaa ctt aat cca cct 198
Leu Ser Asp Ala Ala Val Asn Leu Gln Val Ala Lys Leu Asn Pro Pro
20 25 30

cca gaa gct ctt gca gcc aag ttg gaa gtg aag cac tgc acc gat cag 246
Pro Glu Ala Leu Ala Ala Lys Leu Glu Val Lys His Cys Thr Asp Gln
35 40 45

ata tct ttt aag aaa cga ctc tca ttg gaa aaa gtc ctg gtg gaa ata 294
Ile Ser Phe Lys Lys Arg Leu Ser Leu Glu Lys Val Leu Val Glu Ile
50 55 60

gtg aaa aaa tgt ggt gtg tgacatgtaa aaatgctcaa cctgggtttcc 342
Val Lys Lys Cys Gly Val
65

aaagtctttc aacgacaccc tgatcttcac taaaaattgt aaagggtttca acacgttgct 402

ttaataaaatc acttgccctg cacatcaaaa a 433

<210> 2
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Met Arg Leu Ser Val Cys Leu Leu Met Val Ser Leu Ala Leu Cys Cys
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Tyr Gln Ala His Ala Leu Val Cys Pro Ala Val Ala Ser Glu Ile Thr
-5 -1 1 5 10

Val Phe Leu Phe Leu Ser Asp Ala Ala Val Asn Leu Gln Val Ala Lys
15 20 25

Leu Asn Pro Pro Pro Glu Ala Leu Ala Ala Lys Leu Glu Val Lys His
30 35 40

Cys Thr Asp Gln Ile Ser Phe Lys Lys Arg Leu Ser Leu Glu Lys Val
45 50 55

Leu Val Glu Ile Val Lys Lys Cys Gly Val
60 65

<210> 3
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 Met Lys Leu Ser Val
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tgt ctc ctg ctg gtc acg ctg gcc ctc tgc tgc tac cag gcc aat gcc 102
 Cys Leu Leu Leu Val Thr Leu Ala Leu Cys Cys Tyr Gln Ala Asn Ala
 -15 -10 -5 -1

gag ttc tgc cca gct ctt gtt tct gag ctg tta gac ttc ttc ttc att 150
 Glu Phe Cys Pro Ala Leu Val Ser Glu Leu Leu Asp Phe Phe Phe Ile
 1 5 10 15

agt gaa cct ctg ttc aag tta agt ctt gcc aaa ttt gat gcc cct ccg 198
 Ser Glu Pro Leu Phe Lys Leu Ser Leu Ala Lys Phe Asp Ala Pro Pro
 20 25 30

gaa gct gtt gca gcc aag tta gga gtg aag aga tgc acg gat cag atg 246
 Glu Ala Val Ala Ala Lys Leu Gly Val Lys Arg Cys Thr Asp Gln Met
 35 40 45

tcc ctt cag aaa cga agc ctc att gcg gaa gtc ctg gtg aaa ata ttg 294
 Ser Leu Gln Lys Arg Ser Leu Ile Ala Glu Val Leu Val Lys Ile Leu
 50 55 60

aag aaa tgt agt gtg tgacatgtaa aaactttcat cctggtttcc actgtctttc 349
 Lys Lys Cys Ser Val
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aatgacaccc tgatcttcac tgcagaatgt aaagggtttca acgtcttgct ttaataaatc 409

acttgctctc caaaaaaaaa aaaaaaa 436

<210> 4

<211> 90
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<400> 4

Met Lys Leu Ser Val Cys Leu Leu Leu Val Thr Leu Ala Leu Cys Cys
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Tyr Gln Ala Asn Ala Glu Phe Cys Pro Ala Leu Val Ser Glu Leu Leu
 -5 -1 1 5 10

Asp Phe Phe Phe Ile Ser Glu Pro Leu Phe Lys Leu Ser Leu Ala Lys
 15 20 25

Phe Asp Ala Pro Pro Glu Ala Val Ala Ala Lys Leu Gly Val Lys Arg
 30 35 40

Cys Thr Asp Gln Met Ser Leu Gln Lys Arg Ser Leu Ile Ala Glu Val
 45 50 55

Leu Val Lys Ile Leu Lys Lys Cys Ser Val
 60 65

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 Met Lys Leu Leu
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atg gtc ctc atg ctg gcg gcc ctc ctc ctg cac tgc tat gca gat tct 105
Met Val Leu Met Leu Ala Ala Leu Leu Leu His Cys Tyr Ala Asp Ser
-15 -10 -5

ggc tgc aaa ctc ctg gag gac atg gtt gaa aag acc atc aat tcc gac 153
Gly Cys Lys Leu Leu Glu Asp Met Val Glu Lys Thr Ile Asn Ser Asp
-1 1 5 10 15

ata tct ata cct gaa tac aaa gag ctt ctt caa gag ttc ata gac agt 201
Ile Ser Ile Pro Glu Tyr Lys Glu Leu Leu Gln Glu Phe Ile Asp Ser
20 25 30

gat gcc gct gca gag gct atg ggg aaa ttc aag cag tgt ttc ctc aac 249
Asp Ala Ala Ala Glu Ala Met Gly Lys Phe Lys Gln Cys Phe Leu Asn
35 40 45

cag tca cat aga act ctg aaa aac ttt gga ctg atg atg cat aca gtg 297
Gln Ser His Arg Thr Leu Lys Asn Phe Gly Leu Met Met His Thr Val
50 55 60

tac gac agc att tgg tgt aat atg aag agt aat taactttacc caaggcgttt 350
Tyr Asp Ser Ile Trp Cys Asn Met Lys Ser Asn
65 70

ggctcagagg gctacagact atggccagaa ctcactgtgt gattgctaga aaccactttc 410

ttcttgtgtt gctttttatg tgggaactgc tagacaactg ttgaaacctc aattcattcc 470

atttca 476

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<212> PRT
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<400> 6

Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Leu Leu His Cys
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Tyr Ala Asp Ser Gly Cys Lys Leu Leu Glu Asp Met Val Glu Lys Thr
-5 -1 1 5 10

Ile Asn Ser Asp Ile Ser Ile Pro Glu Tyr Lys Glu Leu Leu Gln Glu
15 20 25

Phe Ile Asp Ser Asp Ala Ala Ala Glu Ala Met Gly Lys Phe Lys Gln
30 35 40

Cys Phe Leu Asn Gln Ser His Arg Thr Leu Lys Asn Phe Gly Leu Met
45 50 55

Met His Thr Val Tyr Asp Ser Ile Trp Cys Asn Met Lys Ser Asn
60 65 70

<210> 7
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<400> 7
cgcgcatgct tgtctgccca gctg 24

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<400> 8
cgcccatgga gttctgccca gctc 24

<210> 9
<211> 24
<212> DNA
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<220>
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<400> 9
cgcgcatgca ctgctatgca gatt 24

<210> 10
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<212> DNA
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<400> 10
cgcaagcttc atttttacat gtca 24

<210> 11
<211> 24

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 <400> 11
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 <400> 12
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 <400> 13
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 <210> 15
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<210> 16
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<400> 16
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<210> 17
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<400> 17
cgcggtacca cgccttgggt aaagtta 27

<210> 18
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<400> 18
cgcggtacca cgccttgggt aaagtta 27

<210> 19
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<400> 19
cgcggtacca ccatggtctc gctggccctt 30

<210> 20
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 <400> 21
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 <210> 22
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 <210> 23
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 <212> DNA
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 <220>
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 <400> 23
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 <210> 24
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Primer_Bind
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<400> 24
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54

<210> 25
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<400> 25

Ile Glu Leu Ser Leu Cys Leu Leu Ile Met Leu Ala Val Cys Cys Tyr
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Glu Ala Asn Ala Ser Gln Ile Cys Glu Leu Val Ala His Glu Thr Ile
 20 25 30

Ser Phe Leu Met Lys Ser Glu Glu Glu Leu Lys Lys Glu Leu Glu Met
 35 40 45

Tyr Asn Ala Pro Pro Ala Ala Val Glu Ala Lys Leu Glu Val Lys Arg
 50 55 60

Cys Val Asp Gln Met Ser Asn Gly Asp Arg Leu Val Val Ala Glu Thr
 65 70 75 80

Leu Val Tyr Ile Phe Leu Glu Cys Gly Val
 85 90

<210> 26
 <211> 90
 <212> PRT
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<400> 26

Ile Glu Leu Ser Leu Cys Leu Leu Ile Met Leu Ala Val Cys Cys Tyr
 1 5 10 15

Glu Ala Asn Ala Ser Gln Ile Cys Glu Leu Val Ala His Glu Thr Ile
 20 25 30

Ser Phe Leu Met Lys Ser Glu Glu Glu Leu Lys Lys Glu Leu Glu Met
 35 40 45

Tyr Asn Ala Pro Pro Ala Ala Val Glu Ala Lys Leu Glu Val Lys Arg
 50 55 60

Cys Val Asp Gln Met Ser Asn Gly Asp Arg Leu Val Val Ala Glu Thr
 65 70 75 80

Leu Val Tyr Ile Phe Leu Glu Cys Gly Val
 85 90

<210> 27
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 <212> PRT
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<400> 27

Met Lys Leu Val Phe Leu Phe Leu Leu Val Thr Ile Pro Ile Cys Cys
 1 5 10 15

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 20 25 30

Thr Ile Asn Ser Thr Val Thr Leu His Asp Tyr Met Lys Leu Val Lys
 35 40 45

Pro Tyr Val Gln Ala His Phe Thr Glu Lys Ala Val Lys Gln Phe Lys
 50 55 60

Gln Cys Phe Leu Asp Gln Thr Asp Lys Thr Leu Glu Asn Val Gly Val
 65 70 75 80

Met Met Glu Ala Ile Phe Asn Ser Glu Ser Cys Gln Gln Pro Ser
 85 90 95